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OM protein - protein search, using sw model

Run on: October 12, 2004, 09:34:09 ; Search time 23 Seconds
(Without alignments)
44.892 Million cell updates/sec

Title: US-10-619-910-11
Perfect score: 111
Sequence: 1 INPETVPKCCAPQNLNALS 20

Scoring table: BILOSTM62
Gapop 10.0 , Gapext 0.5

Searched:
389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cggn_6/ptodata/2/iaa/5A_COMB_pep: *
2: /cggn_6/ptodata/2/iaa/5B_COMB_pep: *
3: /cggn_6/ptodata/2/iaa/6A_COMB_pep: *
4: /cggn_6/ptodata/2/iaa/6B_COMB_pep: *
5: /cggn_6/ptodata/2/iaa/PCFTUS_COMB_PeP: *
6: /cggn_6/ptodata/2/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	100.0	20	4	US-09-439-779B-11
2	111	100.0	102	1	US-08-335-533C-47
3	111	100.0	102	2	US-08-288-18
4	111	100.0	102	3	US-08-478-07A-15
5	111	100.0	102	3	US-08-389-23B-27
6	111	100.0	102	3	US-09-054-536B-27
7	111	100.0	102	3	US-08-931-838B-161
8	111	100.0	102	3	US-08-981-739-161
9	111	100.0	102	3	US-08-203A-1
10	111	100.0	102	4	US-09-128-036-161
11	111	100.0	102	4	US-09-495-308-16
12	111	100.0	102	4	US-09-320-636-161
13	111	100.0	102	4	US-09-374-938C-55
14	111	100.0	104	1	US-07-764-731B-8
15	111	100.0	117	4	US-09-374-938C-69
16	111	100.0	118	1	US-08-481-337-12
17	111	100.0	118	2	US-08-491-835-10
18	111	100.0	118	3	US-09-153-733A-12
19	111	100.0	118	3	US-08-046-032A-10
20	111	100.0	118	3	US-09-172-062-10
21	111	100.0	118	4	US-09-301-530D-10
22	111	100.0	118	4	US-09-369-735-12
23	111	100.0	118	5	PCT-US94-00366-12
24	111	100.0	119	1	PCT-US94-00385-10
25	111	100.0	119	1	US-08-581-539B-12
26	111	100.0	119	1	US-08-555-539-18
27	111	100.0			US-08-08-525-536B-22

ALIGNMENTS

RESULT 1
US-09-439-779B-11

; Sequence 11, Application US/09439779B
; Patent No. 6617307
; GENERAL INFORMATION:
; APPLICANT: Kyocera Corporation
; APPLICANT: Nishimura, Yoshihiko
; APPLICANT: Suzuki, Yoshihisa
; APPLICANT: Tamihara, Masao
; TITLE OF INVENTION: A Peptide and Osteogenetic Accelerator
; FILE REFERENCE: 81918-001
; CURRENT APPLICATION NUMBER: US/09/439, 779B
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; TYPE: PRT
; LENGTH: 20
; SEQ ID NO: 11
; OTHER INFORMATION:
; ORGANISM: Artificial Sequence
; FEATURE: PEPTIDE
; OTHER INFORMATION: :

US-09-439-779B-11

Query Match: 100.0%; Score: 111; DB: 4; Length: 20;
Best Local Similarity: 100.0%; Pred. No.: 8.4e-03; Indels: 0; Gaps: 0;
Matches: 20; Conservative: 0; Mismatches: 0;

QY 1 INPETVPKCCAPQNLNALS 20
Db 1 INPETVPKCCAPQNLNALS 20

RESULT 2
US-08-335-533C-47

; Sequence 47, Application US/08335583C
; Patent No. 5693779
; GENERAL INFORMATION:
; APPLICANT: Moos Jr., Malcolm
; APPLICANT: Wang, Showan
; APPLICANT: Krinks, Marie
; TITLE OF INVENTION: PRODUCTION AND USE OF
; TITLE OF INVENTION: ANTI-DORSALIZING MORPHOGENETIC PROTEIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatibile
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/335, 583C
 FILING DATE: 09-JUN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E.
 REGISTRATION NUMBER: 34, 115
 REFERENCE/DOCKET NUMBER: NPH104.001A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 714-760-0404
 TELEX:
 TELEFAX: 714-760-9502
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 TYPE: amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: C-terminal
 ORIGINAL SOURCE:
 US-08-335-583C-47

RESULT 3
 US-08-288-508C-18
 Sequence 18, application US/08288508C
 Patient No. 5994094
 GENERAL INFORMATION:
 APPLICANT: Hettner, Gertrud
 APPLICANT: Neidhardt, Helge
 APPLICANT: Paulista, Michael
 TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATING FACTOR OF TITLE OF INVENTION: THE TGF-
 FAMILY
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PARENT ADMINISTRATOR; TESTA, HURWITZ &
 STREET: 125 HIGH STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02110

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #11.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/478, 097A
 FILING DATE: 10-AUG-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER ESO, EDMUND R
 REGISTRATION NUMBER: 27, 829
 REFERENCE/DOCKET NUMBER: CRP-080

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7000
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1.102

APPLICATION NUMBER: DE P 44 18 222.8
 FILING DATE: 25-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 44 20 157.5
 FILING DATE: 09-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: JARNS, Kristina M.
 REGISTRATION NUMBER: P 41, 092
 REFERENCE/DOCKET NUMBER: P564-4019
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5000
 TELEFAX: (202) 638-4810
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 TYPE: amino acid
 TOPOLGY: linear
 MOLECULE TYPE: protein
 US-08-288-508C-18
 Query Match 100.0%; Score 111; DB 1; Length 102;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 INPETVVKPCCAPTQLNAlS 20
 ||||| ||||| ||||| ||||| |||||
 Db 57 INPBTVPKPCCAPTQLNAlS 76

RESULT 4
 US-08-478-097A-16
 Sequence 15, Application US/08478097A
 Patient No. 6040431
 GENERAL INFORMATION:
 APPLICANT: KECK, PETER
 APPLICANT: SMART, JOHN
 TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PARENT ADMINISTRATOR; TESTA, HURWITZ &
 STREET: 125 HIGH STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02110

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #11.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/478, 097A
 FILING DATE: 10-AUG-1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER ESO, EDMUND R
 REGISTRATION NUMBER: 27, 829
 REFERENCE/DOCKET NUMBER: CRP-080

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7000
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1.102

; OTHER INFORMATION: /note= "TOP-1 SEQUENCE"

; US-08-478-097A-16

Query Match 100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETVPKCCAPTOINAIS 20
Db 57 INPETVPKCCAPTOINAIS 76

RESULT 5

; Sequence 27, Application US/08289222E

; Patent No. 6120760

; GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HEIGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: FOHL, JENS

APPLICANT: POHL, JENS

TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B

TITLE OF INVENTION: FAMILY

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKATO, MARMELSTEIN, MURRAY & ORAM LLP

STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-289,222E

FILING DATE: 25-AUG-1999

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITTS, MONICA CHIN

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-8005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/38-4910

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4910

INFORMATION FOR SEQ ID NO: 27:

QY 1 INPETVPKCCAPTOINAIS 20
Db 57 INPETVPKCCAPTOINAIS 76

RESULT 6

; Sequence 27, Application US/09054526B

; Patent No. 619550

; GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HEIGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: FOHL, JENS

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKARIO, MARMELSTEIN, MURRAY & ORAM LLP

STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,526B

FILING DATE: 03-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITTS, MONICA CHIN

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-8005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/38-4910

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4910

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-289-222E-27

Query Match 100.0%; Score 111; DB 3; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-08-910-816B-161
Sequence 151, Application US/08931858E

PATENT NO. 6222022

GENERAL INFORMATION:

APPLICANT: JOHNSON, EUGENE M
MILBRANDT, JEFFREY D
KOTZBAUER, PAUL T
LAMPE, PATRICIA A
KLEIN, ROBERT
DESJARLAIS, FRED

APPLICANT: HOWELL & HAFFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 239
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105

FILING DATE: <Unknown>

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 161:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 161:
US-08-931-858E-161

RESULT 8
US-08-981-739-161

Sequence 161, Application US/08981739
Patent No. 6233598

GENERAL INFORMATION:

APPLICANT: KECK, PETER
APPLICANT: GRIFFITH, DIANA L
APPLICANT: CARLSON, WILLIAM D
APPLICANT: RUGER, DAVID C
APPLICANT: SAMPATH, KUBER T

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
TITLE OF INVENTION: MORPHOGEN ANALOGS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/03461
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971613

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 161:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 161:
US-08-981-739-161

RESULT 9
US-08-786-284A-1

Sequence 1, Application US/08786284A
Patent No. 6233598

GENERAL INFORMATION:

APPLICANT: KECK, PETER
APPLICANT: GRIFFITH, DIANA L
APPLICANT: CARLSON, WILLIAM D
APPLICANT: RUGER, DAVID C
APPLICANT: SAMPATH, KUBER T

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
TITLE OF INVENTION: MORPHOGEN ANALOGS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: INC.
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/786,284A
FILING DATE:
CLASSIFICATION: 364

ATTORNEY/AGENT INFORMATION:

NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829

REFERENCE/DOCKET NUMBER: CEP-102

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-0992

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..102
 OTHER INFORMATION: /product= "hOP-1"
 US-08-786-284A-1

Query Match 100.0%; Score 111; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETYVKPCCAPTQLNAlS 20
 Db 57 INPETYVKPCCAPTQLNAlS 76

RESULT 10
 US-09-128-026-161
 Sequence 161, Application US/09128026
 GENERAL INFORMATION:
 PATENT NO. 6,033,355
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR; TESTA, HURWITZ &
 ADDRESSEE: TIBEAULT, LILIP
 STREET: 125 HIGH STREET
 CITY: BOSTON
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09/478,097
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/478,097
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER, EDWARD R
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: STK-059CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7000
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..102
 OTHER INFORMATION: /note= "OP-1 SEQUENCE"
 US-09-496-398-161

Query Match 100.0%; Score 111; DB 4; Length 102;
 Best Local Similarity 100.0%; Pred. No. 4.3e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETYVKPCCAPTQLNAlS 20
 Db 57 INPETYVKPCCAPTQLNAlS 76

RESULT 12
 US-09-220-616-161
 Sequence 161, Application US/09220616
 PATENT NO. 6,645,337
 GENERAL INFORMATION:
 APPLICANT: JOHNSON JR., EUGENE M.
 APPLICANT: MILBRANDT, JEFFREY D.
 APPLICANT: KOTZBAUER, PAUL T.
 APPLICANT: LAMPE, PATRICIA A.
 TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAERKAMP, L.C.
 STREET: 7733 FORSYTH BOULEVARD, SUITE 1400

RESULT 11

RESULT 11

RESULT 14
US-07-764-731B-8
Sequence 8, Application US/07764731B
; Patent No. 536875
; GENERAL INFORMATION:
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Rosen, Vicki A.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,616
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; NAME: HOLLAND, DONALD R.
; FILING DATE: 31-Aug-1998
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEX/FAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 161:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: peptide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-220-616-161

Query Match 100.0%; Score 111; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETVPRKCCAPTOQNAIS 20
Db 57 INPETVPRKCCAPTOQNAIS 76

RESULT 13
US-09-374-958C-55
; Sequence 55, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: STRYKER Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 55
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: OP-1
; US-09-374-958C-55

Query Match 100.0%; Score 111; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPETVPRKCCAPTOQNAIS 20
Db 57 INPETVPRKCCAPTOQNAIS 76

RESULT 15
US-09-374-958C-69
; Sequence 69, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: STRYKER Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 69
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Trypsin truncated H2223 mutant
; US-09-374-958C-69

Query Match 100.0%; Score 111; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;

Wed Oct 13 07:00:28 2004

usb-10-619-910-11.rai

Page 7

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 INPETVPRPCATQNAIS 20
Db 72 INPETVPRCCAPTQNAIS 91

Search completed: October 12, 2004, 09:38:46
Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 09:37:49 ; Search time 95 Seconds
(without alignments)
6.7041 Million cell updates/sec

Title: score:
Perfect score:
Sequence: 1 INPETVPKPCCATQNLNALS 20

Scoring table: BLOSUM62
Gapcr 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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19: /cgn2_6/podata/1/pubpaal/US09_PUBCOMB.pep:*

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29: /cgn2_6/podata/1/pubpaal/US09_PUBCOMB.pep:*

30: /cgn2_6/podata/1/pubpaal/US08_PUBCOMB.pep:*

31: /cgn2_6/podata/1/pubpaal/US07_PUBCOMB.pep:*

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33: /cgn2_6/podata/1/pubpaal/US05_PUBCOMB.pep:*

34: /cgn2_6/podata/1/pubpaal/US04_PUBCOMB.pep:*

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36: /cgn2_6/podata/1/pubpaal/US02_PUBCOMB.pep:*

37: /cgn2_6/podata/1/pubpaal/US01_PUBCOMB.pep:*

38: /cgn2_6/podata/1/pubpaal/US00_PUBCOMB.pep:*

39: /cgn2_6/podata/1/pubpaal/US09_PUBCOMB.pep:*

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41: /cgn2_6/podata/1/pubpaal/US07_PUBCOMB.pep:*

42: /cgn2_6/podata/1/pubpaal/US06_PUBCOMB.pep:*

43: /cgn2_6/podata/1/pubpaal/US05_PUBCOMB.pep:*

44: /cgn2_6/podata/1/pubpaal/US04_PUBCOMB.pep:*

45: /cgn2_6/podata/1/pubpaal/US03_PUBCOMB.pep:*

RESULT 1
US-10-619-910-11

; Sequence 11, Application US/101619910

; Publication No. US20040053844A1

; GENERAL INFORMATION:

; APPLICANT: Kyocera Corporation

; APPLICANT: Nishimura, Yoshinori

; APPLICANT: Suzuki, Yoshihisa

; APPLICANT: Tanihara, MasaO

; TITLE OF INVENTION: A Peptide and Osteogenic Accelerator

; FILE REFERENCE: 81918-0001

; CURRENT APPLICATION NUMBER: US/10/619 910

; CURRENT FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: US/09/439,779B

; PRIOR FILING DATE: 2001-09-10

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 11

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: :

; US-10-619-910-11

Query Match 100.0%; Score 111; DB 12; length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETVPKPCCATQNLNALS 20

D 1 INPETVPKPCCATQNLNALS 20

RESULT 2
US-09-752-831A-39
; Sequence 39, Application US/03754831A

; Publication No. US20030228345A1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query

Match Length

DB ID

Description

Result No.	Score	Match Length	DB ID	Description
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2	111	100.0	97	US-09-791-966-1
3	111	100.0	102	US-09-791-966-1
4	111	100.0	102	US-10-187-94-16
5	111	100.0	102	US-10-164-79-4
6	111	100.0	107	US-09-754-831A-9
7	111	100.0	112	US-09-813-398-30
8	111	100.0	118	US-10-115-4-06-10
9	111	100.0	118	US-10-154-33-12
10	111	100.0	118	US-10-704-223-10
11	111	100.0	119	US-09-813-429-13
12	111	100.0	119	US-09-859-211-40
13	111	100.0	119	US-09-880-708-18
14	111	100.0	119	US-09-882-556-40
15	111	100.0	12	US-10-463-973-40

GENERAL INFORMATION:
 APPLICANT: Oppermann, Herman
 APPLICANT: Kubrasampath, Thangavel
 APPLICANT: Rueger, David
 APPLICANT: Ozkaynak, Engin
 TITLE OF INVENTION: Osteogenic devices
 FILE REFERENCE: STK-08CN
 CURRENT APPLICATION NUMBER: US/09/754, 831A
 PRIOR APPLICATION NUMBER: US 08/375, 901
 PRIOR FILING DATE: 1998-01-20
 PRIOR APPLICATION NUMBER: US 08/145, 812
 PRIOR FILING DATE: 1993-11-01
 PRIOR APPLICATION NUMBER: US 07/995, 345
 PRIOR FILING DATE: 1992-12-22
 PRIOR APPLICATION NUMBER: US 07/315, 342
 PRIOR FILING DATE: 1989-02-23
 PRIOR APPLICATION NUMBER: US 07/232, 630
 PRIOR FILING DATE: 1988-08-15
 PRIOR APPLICATION NUMBER: US 07/179, 406
 PRIOR FILING DATE: 1988-04-08
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 39
 LENGTH: 97
 TYPE: PRT
 ORGANISM: mammalian
 FEATURE: OTHER INFORMATION: OPI shorter sequence capable of inducing endochondral bone formation
 US-09-754-831A-39

Query Match 100.0%; Score 111; DB 11; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.3e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 INPBETVPKCCAPTOLNAlS 20
 Db 52 INPBETVPKCCAPTOLNAlS 71

RESULT 3
 US-09-791-946-1
 ; Sequence 1, Application US/09791946
 ; Patent No. US2002028453A1
 GENERAL INFORMATION:
 APPLICANT: KECK, PETER
 GRIFFITH, DIANA L
 CARLSON, WILLIAM D
 RUEGER, DAVID C
 SAMPATH, KUBER T
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCING
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
 ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURNITZ &
 STREET: 125 HIGH STREET
 CITY: BOSTON
 STATE: MA
 COUNTY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/187,394
 FILING DATE: 28-JUNE-2002
 CLASSIFICATION: 28-
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/496,398
 FILING DATE: 02-FEB-2000
 CLASSIFICATION: 28-
 APPLICATION NUMBER: US 08/478,097
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 28-
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER ESQ, EDMUND R
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: STK-059CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7100
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:

ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER, EDMUND R
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: CRRP-102
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (508) 435-9001
 TELEFAX: (508) 435-0992
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 102 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..102
 OTHER INFORMATION: /product= "RQP-1"
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-791-946-1
 Query Match 100.0%; Score 111; DB 9; Length 102;
 Best Local Similarity 100.0%; Pred. No. 3.5e-07; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 Qy 1 INPBETVPKCCAPTOLNAlS 20
 Db 57 INPBETVPKCCAPTOLNAlS 76

RESULT 4
 US-10-187-394-16
 ; Sequence 16, Application US/10187394
 ; Publication No. US20030175667A1
 GENERAL INFORMATION:
 APPLICANT: KECK, PETER
 APPLICANT: SMART, JOHN
 TITLE OF INVENTION: SINGLE CHAIN ANALOGS OF TGF-B
 TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURNITZ &
 ADDRESSEE: THIBEAUT, ILIP
 STREET: 125 HIGH STREET
 CITY: BOSTON
 STATE: MA
 COUNTY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/187,394
 FILING DATE: 28-JUNE-2002
 CLASSIFICATION: 28-
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/496,398
 FILING DATE: 02-FEB-2000
 CLASSIFICATION: 28-
 APPLICATION NUMBER: US 08/478,097
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 28-
 ATTORNEY/AGENT INFORMATION:
 NAME: PITCHER ESQ, EDMUND R
 REGISTRATION NUMBER: 27,829
 REFERENCE/DOCKET NUMBER: STK-059CN
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7100
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:

LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: Protein
; LOCATION: 1..102
; OTHER INFORMATION: /note= "OP-1 SEQUENCE"
; US-10-187-394-16

Query Match Similarity 100.0%; Score 111; DB 14; Length 102;
; Best Local Similarity 100.0%; Pred. No. 3.5e-07; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;

Qy 1 INPETVPPCPCAPTOINAI S 20
Db 57 INPETVPPCPCAPTOINAI S 76

RESULT 5
US-10-164-279-4
; Sequence 4, Application US/10164279
; Publication No. US20030185792A1
; GENERAL INFORMATION:
; APPLICANT: Keck, P
; TITLE OF INVENTION: MORPHOGEN ANALOGS OF BOND MORPHOGENIC PROTEINS
; FILE REFERENCE: CIBT-P04-566
; CURRENT APPLICATION NUMBER: US/10/164-279
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 09/791946
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 4
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-164-279-4

Query Match Similarity 100.0%; Score 111; DB 14; Length 102;
; Best Local Similarity 100.0%; Pred. No. 3.5e-07; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;

Qy 1 INPETVPPCPCATQINAI S 20
Db 57 INPETVPPCPCAPTOINAI S 76

RESULT 6
US-09-754-831A-9
; Sequence 9, Application US/09754831A
; Publication No. US20030228345A1
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Herman
; APPLICANT: Kuberaswamy, Thangavel
; APPLICANT: Rueger, David
; APPLICANT: Ozkaynak, Engin
; TITLE OF INVENTION: Osteogenic Devices
; FILE REFERENCE: SIK-080N
; CURRENT APPLICATION NUMBER: US/09/754, 831A
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: US 08/375, 901
; PRIOR FILING DATE: 1995-01-20
; PRIOR APPLICATION NUMBER: US 08/145, 812
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 07/995, 345
; PRIOR FILING DATE: 1992-12-22
; PRIOR APPLICATION NUMBER: US 07/315, 342
; PRIOR FILING DATE: 1989-02-23
; PRIOR APPLICATION NUMBER: US 07/232, 630
; PRIOR FILING DATE: 1989-08-15
; PRIOR APPLICATION NUMBER: US 07/179, 406
; PRIOR APPLICATION NUMBER: US 07/179, 406

Query Match Similarity 100.0%; Score 111; DB 14; Length 102;
; Best Local Similarity 100.0%; Pred. No. 3.5e-07; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;

Qy 1 INPETVPPCPCAPTOINAI S 20
Db 57 INPETVPPCPCAPTOINAI S 76

RESULT 7
US-09-813-398-30
; Sequence 30, Application US/09813398
; Publication No. US20030169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Marusz W. Szrudlinski
; TITLE OF INVENTION: CYSTEINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: U0FMD.003CI
; CURRENT APPLICATION NUMBER: US/09/813, 398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-813-398-30

Query Match Similarity 100.0%; Score 111; DB 9; Length 112;
; Best Local Similarity 100.0%; Pred. No. 3.8e-07; Indels 0; Gaps 0;
; Matches 20; Conservative 0; Mismatches 0;

Qy 1 INPETVPPKCCAPTOINAI S 20
Db 68 INPETVPPKCCAPTOINAI S 87

RESULT 8
US-10-115-406-10
; Sequence 10, Application US/10115406
; Publication No. US20020127612A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: LEE, Se-Jin
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
; FILE REFERENCE: JHU1190-3
; CURRENT APPLICATION NUMBER: US/10/115, 406
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/301, 520
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: US 09/172, 062
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/491, 835
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: PCT/US94/00685
; PRIOR FILING DATE: 1994-01-12
; PRIOR APPLICATION NUMBER: US 08/003, 303

PRIOR FILING DATE: 1993-01-12
 NUMBER OF SEQ ID NOS: 28
 SEQ ID NO: 10
 LENGTH: 118
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-115-406-10

RESULT 9
 US-10-154-333-12
 Sequence 12, Application US/10154333
 Publication No. US20030109684A1.
 GENERAL INFORMATION:
 APPLICANT: JOHNS HOPKINS UNIVERSITY
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-3
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
 STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
 CITY: LOS ANGELES
 STATE: CALIFORNIA
 COUNTRY: US
 ZIP: 90067

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/154,333
 FILING DATE: 21-MAY-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/389,705
 FILING DATE: 03-SEP-1999
 APPLICATION NUMBER: 09/153,733
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: WETHERELL, JR., PH.D., JOHN R.
 REGISTRATION NUMBER: 31,678
 REFERENCE/DOCKET NUMBER: FD2279 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5100
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 118 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: OP-1
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..118

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
 US-10-154-333-12

Query Match 100.0%; Score 111; DB 13; Length 118;
 Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Mismatches 20;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 US-10-704-223-10
 Sequence 10, Application US/10704223
 Publication No. US20040152143A1.
 GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-9
 FILE REFERENCE: JHU190-7
 CURRENT APPLICATION NUMBER: US/10/704,223
 PRIOR FILING DATE: 2003-11-07
 PRIOR APPLICATION NUMBER: US 10/115,406
 PRIOR FILING DATE: 2002-04-02
 PRIOR APPLICATION NUMBER: US 09/301,520
 PRIOR FILING DATE: 1999-04-28
 PRIOR APPLICATION NUMBER: US 09/172,062
 PRIOR FILING DATE: 1998-10-13
 PRIOR APPLICATION NUMBER: US 08/491,835
 PRIOR FILING DATE: 1995-10-23
 PRIOR APPLICATION NUMBER: PCT/US94/00685
 PRIOR FILING DATE: 1994-01-12
 PRIOR APPLICATION NUMBER: US 08/003,303
 PRIOR FILING DATE: 1993-01-12
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 10
 LENGTH: 118
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-704-223-10

RESULT 11
 US-09-813-459-13
 Sequence 13, Application US/09813459
 Patent No. US20020107369A1
 GENERAL INFORMATION:
 APPLICANT: Lee, Se-Jin
 Cunningham, No. US20020107369A1
 TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-10
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Spensley Horn Jubas & Lubitz
 STREET: 1880 Century Park East, Suite 500
 CITY: Los Angeles
 STATE: California
 COUNTRY: USA
 ZIP: 90067

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/813,459
 FILING DATE: 20-Mar-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/624,635
 FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Weherell, Jr., Ph.D., John R.,
 REGISTRATION NUMBER: 31-678
 REFERENCE/DOCKET NUMBER: PD-3054

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5110
 TELEFAX: (619) 455-5100
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: OP-1

FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..119
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Query Match 100.0%; Score 111; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative

Qy 1 INPETYVKPCAPQNLNS 20
 Db 74 INPETYVKPCAPQNLNS 93

RESULT 12
 US-09-859-211-40
 Sequence 40, Application US/09859211
 ; Patent No. US2002017125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Se-Jin
 ; ATTORNEY: McPherron, Alexandra C.
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8
 ; FILE REFERENCE: 07265/144001
 ; CURRENT APPLICATION NUMBER: US/09/859,211
 ; CURRENT FILING DATE: 2001-05-15
 ; PRIOR APPLICATION NUMBER: 09/019,070
 ; PRIOR FILING DATE: 1998-02-05
 ; PRIOR APPLICATION NUMBER: 08/862,445
 ; PRIOR FILING DATE: 1997-05-23
 ; PRIOR APPLICATION NUMBER: 08/847,910
 ; PRIOR FILING DATE: 1997-04-28
 ; PRIOR APPLICATION NUMBER: 08/795,071
 ; PRIOR FILING DATE: 1997-02-05
 ; PRIOR APPLICATION NUMBER: 08/552,596
 ; PRIOR FILING DATE: 1995-10-26
 ; PRIOR APPLICATION NUMBER: PCT/US94/03019
 ; PRIOR FILING DATE: 1994-03-18
 ; PRIOR APPLICATION NUMBER: 08/033,923
 ; PRIOR FILING DATE: 1993-03-19
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 40
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-859-211-40

Query Match 100.0%; Score 111; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative

Qy 1 INPETYVKPCAPQNLNS 20
 Db 74 INPETYVKPCAPQNLNS 93

RESULT 13
 US-09-880-708-18
 Sequence 18, Application US/09880708
 ; Patent No. US2002016561A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Se-Jin
 ; ATTORNEY: Huynh, Thanh
 ; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-5
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
 ; STREET: 4165 Executive Drive, Suite 1600
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121-2189

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows95
 SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,708
 FILING DATE: 12-Jun-2001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/145,060
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/003,144
 FILING DATE: 12-Jan-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Lisa A. Haile, Ph.D.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/057002

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 858/677-1456
 TELEFAX: 619/677-1465
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 IMMEDIATE SOURCE:
 CLONE: OP-1

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match 100.0%; Score 111; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative

Qy 1 INPETYVKPCAPQNLNS 20
 Db 74 INPETYVKPCAPQNLNS 93

RESULT 14
 US-09-872-856-40
 Sequence 40, Application US/09872856
 ; Publication No. US200300746804
 ; GENERAL INFORMATION:
 ; APPLICANT: Johns Hopkins University School of Medicine
 ; ATTICANT: Lee, Se-Jin
 ; ATTICANT: McPherron, Alexandra
 ; TITLE OF INVENTION: Growth Differentiation Factor-8
 ; FILE REFERENCE: JHU120-17
 ; CURRENT APPLICATION NUMBER: US/09/872,856
 ; CURRENT FILING DATE: 2001-06-01
 ; PRIOR APPLICATION NUMBER: US 09/124,180
 ; PRIOR FILING DATE: 1998-07-28
 ; PRIOR APPLICATION NUMBER: US 09/019,070
 ; PRIOR FILING DATE: 1998-02-05
 ; PRIOR APPLICATION NUMBER: US 08/862,445

Search completed: October 12, 2004, 09:45:49
 Job time : 97 secs

PRIOR FILING DATE: 1997-05-23
 PRIOR APPLICATION NUMBER: US 08/847,910
 PRIOR FILING DATE: 1997-04-28
 PRIOR APPLICATION NUMBER: US 08/795,071
 PRIOR APPLICATION NUMBER: US 08/525,596
 PRIOR FILING DATE: 1995-10-25
 PRIOR APPLICATION NUMBER: PCT/US 94/03019
 PRIOR FILING DATE: 1994-03-18
 PRIOR APPLICATION NUMBER: US 08/033,923
 PRIOR FILING DATE: 1993-03-19
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 40
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-872-836-40

Query Match 100.0%; Score 111; DB 10; length 119;
 Best local Similarity 100.0%; Pred. No. 4e-07; 0;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy	Db
1 INPETVPKCCAPQNLNALS 20	74 INPETVPKCCAPQNLNALS 93

RESULT 15
 US-10-613-973-40
 Sequence 40, Application US/10463973
 Publication No. US20040055027A1
 GENERAL INFORMATION:
 APPLICANT: Johns Hopkins University School of Medicine
 APPLICANT: Lee, Se-Jin
 APPLICANT: Mapheron, Alexandra
 TITLE OF INVENTION: Growth Differentiation Factor-8
 FILE REFERENCE: JHU120-17
 CURRENT APPLICATION NUMBER: US/10/463,973
 PRIOR APPLICATION NUMBER: US/09/872,856
 PRIOR FILING DATE: 2001-06-01
 PRIOR APPLICATION NUMBER: US 09/124,180
 PRIOR FILING DATE: 1998-07-28
 PRIOR APPLICATION NUMBER: US 09/019,071
 PRIOR FILING DATE: 1998-02-05
 PRIOR APPLICATION NUMBER: US 08/862,445
 PRIOR FILING DATE: 1997-05-23
 PRIOR APPLICATION NUMBER: US 08/847,910
 PRIOR FILING DATE: 1997-04-28
 PRIOR APPLICATION NUMBER: US 08/795,071
 PRIOR FILING DATE: 1997-02-05
 PRIOR APPLICATION NUMBER: US 08/525,596
 PRIOR FILING DATE: 1995-10-25
 PRIOR APPLICATION NUMBER: PCT/US 94/03019
 PRIOR FILING DATE: 1994-03-18
 PRIOR APPLICATION NUMBER: US 08/033,923
 PRIOR FILING DATE: 1993-03-19
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 40
 LENGTH: 119
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-463-973-40

Query Match 100.0%; Score 111; DB 12; length 119;
 Best local Similarity 100.0%; Pred. No. 4e-07; 0;
 Matches 20; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

				Copyright (c) 1993 - 2004 Compugen Ltd.
query:	GenCore version 5.1.6	protein - protein search, using sw model	run on:	October 12, 2004, 09:10:03 ; Search time 30 Seconds
post-processing:	Minimum Match 0%	Maximum Match 100%		(without alignments)
database :	PIR_78:*	Listing first 45 summaries		64.128 Million cell updates/sec
	1: Pirl:*			
	2: Pir2:*			
	3: Pir3:*			
	4: Pir4:*			
total number of hits satisfying chosen parameters:	283366	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and its derived by analysis of the total score distribution.		
result	No.	Score	Query Length	DB ID
				SUMMARIES
				RESULTS
				1
				151284
				bone morphogenetic protein-7 - chicken (fragment)
				C;Species: Gallus gallus (chicken)
				C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 16-Jul-1999
				C;Accession: 151284
				R;Houston, B.; Thorp, B.H.; Burt, D.W.
				J. Mol. Endocrinol. 13, 289-301, 1994
				A;Title: Molecular cloning and expression of bone morphogenetic protein-7 in the chick embryo
				A;Reference number: 151284; PMID:9520473; PMID:7893347
				A;Accession: 151284
				A;Status: Preliminary; translated from GB/EMBL/DDJB
				A;Molecule type: mRNA
				A;Cross-references: GB:S77477; NID:957233; PIDN:AAB33846.1; PID:957234
				C;Superfamily: inhibitor
				Query Match Similarity Score 100.0%; Pred. No. 9.7e-09;
				Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
				Matches 20; Conservative 0;
				Qy
				1 INPSETVPKPCAPTQLNAIS 20
				Db
				268 INPSETVPKPCAPTQLNAIS 287
				RESULT 2
				BMH7
				bone morphogenetic protein-7 precursor - human
				N;Alternate name: osteogenic protein 1
				C;Species: Homo sapiens (man)
				C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
				C;Accession: C39263; S10529
				R;Celeste, A.J.; Iannazzi, J.A.; Taylor, R.C.; Hawick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, R.; Proc. Natl. Acad. Sci. U.S.A. 87, 9843-9847, 1990
				A;Title: Identification of transforming growth factor beta family members present in bone
				A;Reference number: A39263; MUID:91088608; PMID:2263636
				A;Accession: C39263
				A;Molecule type: mRNA
				A;Cross-references: <CELL>
				A;Cross-references: GB:M60316; GB:M3895; NID:939563; PIDN:AA136738.1; PID:939564
				R;Oezkaynak, E.; Ridder, D.C.; Drier, E.A.; Corbett, C.; Ridge, R.J.; Sampath, T.K.; Opi, EMBL J. 9, 2083-2093, 1990
				A;Title: Op-1 cDNA encodes an osteogenic protein in the TGF-beta family.
				A;Reference number: S10529; MUID:90291971; PMID:2357959
				A;Accession: S10529
				A;Molecule type: mRNA
				A;Cross-references: 1431<OEZ>
				A;Residues: 1431<OEZ>
				A;Cross-references: EMBL:X51801; NID:935151; PIDN:CAA36100.1; PID:935152
				C;Genetics:
				A;Gene: BMP7
				A;Cross-references: GDB:127597; OMIM:112267
				ALIGNMENTS
				30 63 55.8 39.6 1 BMHU2
				31 63 56.8 39.8 2 JH0688
				32 63 56.8 39.8 2
				33 63 56.8 49.5 2 S43294
				34 63 56.8 50.1 2 A55452
				35 63 56.8 50.1 2 JC2347
				36 55 49.5 12.5 2 S43295
				37 55 49.5 43.6 2 B55452
				38 54 48.6 2 S01825
				39 54 48.6 41.0 2 A41397
				40 54 48.6 41.0 2 A55706
				41 54 48.6 41.2 2 A36169
				42 54 48.6 41.2 2 A34939
				43 54 48.6 41.3 2 JC4862
				44 54 48.6 41.3 2 JC4646
				45 54 48.6 47.8 2 JC4838

A;Map position: 20pter-20qter
 C;Superfamily: inhibin
 C;Keywords: bone; dimer; glycoprotein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-431/Product: bone morphogenetic protein 7 #status predicted <MAT>
 F;187,302,321,372/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 100%; Score 11; DB 1; Length 431;
 Best Local Similarity 100%; Pred. No. 1.3e-08; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 INPBTVPKPCAPTONAIS 20
 Db 386 INPBTVPKPCAPTONAIS 405

RESULT 3
 JO1184 osteogenic protein 1 precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;ID: 31-Dec-1991 #sequence_change 31-Dec-1991 #text_change 06-Dec-1996
 C;Accession: JO1184; PQ0224
 R;Oezkaynak, E.; Schneegassberg, P.N.J.; Oppermann, H.
 A;Title: Murine osteogenic protein (OP-1); high levels of mRNA in kidney.
 A;Reference number: JO1184; MUID:91354237; PMID:1715687
 A;Molecule type: DNA
 A;Residues: 1-120 <OEZ>
 A;Cross-references: EMBL:X56906
 A;Accession: PQ0224
 A;Molecule type: mRNA
 A;Residues: 54-30 <OEZ>
 C;Comment: This protein induces bone formation.
 C;Superfamily: inhibin
 C;Keywords: glycoprotein
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-430/Product: osteogenic protein-1 #status predicted <MAT>
 F;291-430/Prediction: binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 97.3%; Score 108; DB 2; Length 430;
 Best Local Similarity 95.0%; Pred. No. 3.5e-08; Mismatches 1; Conservative 19; Matches 19; Indels 0; Gaps 0;

Qy 1 INPBTVPKPCAPTONAIS 20
 Db 385 INPBTVPKPCAPTONAIS 404

RESULT 4
 JO10690 bone morphogenetic protein 7 precursor - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Accession: JO10690 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C;Accession: JO10690 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 R;Nishimatsu, S.; Suzuki, A.; Shoda, A.; Murakami, K.; Ueno, N.
 A;Title: Genes for bone morphogenetic proteins are differentially transcribed in early a
 A;Reference number: JO10687; MUID:92378616; PMID:1510675
 A;Accession: JO10690
 A;Molecule type: mRNA
 A;Residues: 1-426 <NTS>
 A;Cross-references: GB:X63427; NID:964591; PIDN:CAA45021.1; PID:964592
 A;Experimental source: oocyte
 C;Superfamily: inhibin
 C;Keywords: glycoprotein
 F;283-426/Product: bone morphogenetic protein 7 #status predicted <MAT>
 F;177,307,367/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 96.4%; Score 107; DB 2; Length 426;
 Best Local Similarity 95.0%; Pred. No. 4.9e-08;

RESULT 5
 S37618 vgr Protein - rat (fragment)
 V;Species: Rattus norvegicus (Norway rat)
 C;ID: 18-Feb-1994 #sequence_revision 26-May-1995 #text_change 16-Jul-1999
 C;Accession: S37618
 R;Sauermann, U.; Meyermann, R.; Schluesener, H.J.
 J;Neurosci. Res. 33, 1421-147, 1992
 A;Title: Cloning of a novel TGF-beta related cytokine, the vgr, from rat brain: cloning & expression
 A;Reference number: S37618; MUID:9308575; PMID:1453478
 A;Accession: S37618
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-207 <SAU>
 A;Cross-references: EMBL:X58830; NID:957475; PIDN:CAA416341; PID:957476
 A;Note: the sequence from Fig. 4 is inconsistent with that from Fig. 1 in having 88-Ser <
 C;Superfamily: inhibin
 Query Match 87.4%; Score 97; DB 2; Length 207;
 Best Local Similarity 85.0%; Pred. No. 7.3e-07; Mismatches 2; Conservative 17; Matches 17; Indels 0; Gaps 0;

Qy 1 INPBTVPKPCAPTONAIS 20
 Db 162 MNPEYVPKCCAPTKNAIS 181

RESULT 6
 A54798 vg-1-related protein precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;ID: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
 C;Accession: A54798; A33925; S7442
 R;Gitelman, S.E.; Kobrin, M.S.; Ye, J.Q.; Lopez, A.R.; Lee, A.; Deryck, R.
 A;Title: Recombinant vgr-1/BMP-6-expressing tumors induce fibrosis and endochondral bone
 A;Reference number: A54798; MUID:94375535; PMID:809189
 A;Accession: A54798
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-510 <GT>
 A;Cross-references: EMBL:X80992; NID:9530729; PIDN:CAA56917.1; PID:9530730
 R;Lyons, K.; Gravar, J.L.; Lee, A.; Hasumi, S.; Lindquist, P.B.; Chen, E.Y.; Hogan, B.L.
 P;Proc. Natl. Acad. Sci. U.S.A. 86, 4554-4558, 1989
 A;Accession: A33925
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-510 <LYO>
 A;Accession: A33925
 A;Title: Vgr-1, a mammalian gene related to Xenopus vg-1, is a member of the transformin
 A;Reference number: A33925
 A;Cross-references: GB:J04566; NID:9202352; PIDN:AAA40548.1; PID:g202353
 C;Superfamily: inhibin
 Query Match 87.4%; Score 97; DB 2; Length 510;
 Best Local Similarity 85.0%; Pred. No. 1.7e-06; Mismatches 2; Conservative 17; Matches 17; Indels 0; Gaps 0;

Qy 1 INPBTVPKPCAPTONAIS 20
 Db 465 MNPEYVPKCCAPTKNAIS 484

RESULT 7
 BMHU6 bone morphogenetic protein 6 precursor - human
 C;Species: Homo sapiens (man)

C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C;Accession: B39263
 R/Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, M.; Reference number: A39263; MUID:91088608; PMID:2263636
 A;Residue type: mRNA
 A;Cross-references: GB:M513 <CBL>
 C;Genetics:
 A;Gene: GDB:BMP5
 A;Cross-references: GDB:127595; OMIM:112265
 A;Map position: 6pter-6qter
 C;Superfamily: inhibin
 C;Keywords: bone; glycoprotein
 C;KeyWords: bone; glycoprotein
 F;1-237/Domain: signal sequence #status predicted <SIG>
 F;1-316/Domain: propeptide #status predicted <PRO>
 F;317-454/Product: bone morphogenetic protein 5 #status predicted <MAT>
 F;211,327,345,395/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 87.4%; Score 97; DB 1; Length 513;
 Best Local Similarity 85.6%; Pred. No. 1.7e-06; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 INPETPKPCAPTONAIS 20
 Db 468 MPPEVPPKPCAPTKNAIS 487

RESULT 8
 I49542
 bone morphogenetic protein 5 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1995 #text_change 16-Jul-1999
 C;Accession: I49542
 R/King, J.A.; Marker, P.C.; Saung, K.J.; Kingsley, D.M.
 Dev. Biol. 166: 112-122, 1994
 A;Title: BMP5 and the molecular, skeletal, and soft-tissue alterations in short ear mice
 A;Reference number: I49542; MUID:95046894; PMID:7958439
 A;Reference: I49542
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-452 <EBS>
 A;Cross-references: GB:L41145; NID:9755033; PIDN:AAA64612.1; PID:9755034
 A;Gene: BMP5
 C;Genetics:
 C;Superfamily: inhibin
 Query Match 78.4%; Score 87; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 4.2e-05; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Indels 0; Gaps 0;
 QY 3 PETVPKPCAPTONAIS 20
 Db 409 PDHVPKPCAPTKNAIS 426

RESULT 9
 BH005
 bone morphogenetic protein 5 precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 18-Oct-1991 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
 C;Accession: A9263
 R/Celeste, A.J.; Iannuzzi, J.A.; Taylor, R.C.; Hewick, R.M.; Rosen, V.; Wang, E.A.; Wozniak, M.; Reference number: A39263; MUID:91088608; PMID:2263636
 A;Residue type: mRNA
 A;Cross-references: GB:M513 <CBL>
 A;Gene: GDB:BMP5
 A;Cross-references: GDB:127595; OMIM:112265
 A;Map position: 6pter-6qter
 C;Superfamily: inhibin
 C;Keywords: bone; glycoprotein
 C;KeyWords: bone; glycoprotein
 F;1-237/Domain: signal sequence #status predicted <SIG>
 F;1-316/Domain: propeptide #status predicted <PRO>
 F;317-454/Product: bone morphogenetic protein 5 #status predicted <MAT>
 F;211,327,345,395/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 78.4%; Score 87; DB 1; Length 454;
 Best Local Similarity 83.3%; Pred. No. 4.3e-05; 1; Mismatches 1; Indels 0; Gaps 0;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PETVPKPCAPTONAIS 20
 Db 411 PDHVPKPCAPTKNAIS 428

RESULT 10
 A36626
 osteogenic protein 18K chain - bovine (fragments)
 C;Species: Bos primigenius taurinus (cattle)
 C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 03-May-1996
 C;Accession: A36626
 R/Rampatti, T.R.; Coughlin, J.E.; Whetstone, R.M.; Banach, D.; Corbett, C.; Ridge, R.J.; J.; Biol. Chem. 265: 1198-1320, 1990
 A;Title: Bovine osteogenic protein is composed of dimers of OP-1 and BMP-2A, two members
 A;Reference number: A36626; MUID:9030665; PMID:2376592
 A;Reference: A36626
 A;Status: preliminary
 A;Accession: A36626
 A;Molecule type: protein
 A;Residues: 1-34 <SAM>
 C;Superfamily: inhibin
 C;Genetics:
 C;Superfamily: inhibin
 Query Match 75.7%; Score 84; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05; 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 INPETVPKPCAPT 14
 Db 21 INPETVPKPCAPT 34

RESULT 11
 A43918
 TGF-beta-related protein 60A precursor - fruit fly (*Drosophila melanogaster*)
 NT;Alternate name: bone morphogenetic protein homolog precursor
 C;Species: Drosophila melanogaster
 C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
 C;Accession: A43918; A41233
 R/Doctor, J.S.; Jackson, P.D.; Rashka, K.B.; Visalli, M.; Hoffmann, F.M.
 Dev. Biol. 151: 491-505, 1992
 A;Title: Sequence, biochemical characterization, and developmental expression of a new member of the transforming growth factor beta family in *Drosophila melanogaster*
 A;Reference number: A43918; MUID:92290120; PMID:1601181
 A;Accession: A43918
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-455 <DOC>
 A;Cross-references: GB:M84795; NID:9156729; PIDN:AAA28307.1; PID:9156730
 A;Note: sequence extracted from NCBI backbone (NCBIN:106399, NCBIPI:106400)
 R/Wharton, K.A.; Thomsen, G.H.; Gebhart, W.M.
 Proc. Natl. Acad. Sci. U.S.A. 88: 9114-9118, 1991
 A;Title: Drosophila gene, another transforming growth factor beta family member, is expressed in the nervous system
 A;Reference number: A41233; MUID:92290121; PMID:124384
 A;Accession: A41233
 A;Molecule type: mRNA
 A;Residue: 1-455 <WHA>
 A;Cross-references: GB:M77012; NID:9156727; PIDN:AAA28306.1; PID:9156728
 C;Comment: This protein is a member of the transforming growth factor beta family.
 A;Gene: 60A
 C;Genetics:
 C;Cross-references: FlyBase:FBgn0024234

C;Superfamily: inhibin
C;Keywords: homodimer

Query Match 69.4%; Score 77; DB 2; Length 455;
Best Local Similarity 63.2%; Pred. No. 0.0012; Mismatches 3; Indels 0; Gaps 0;

Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPETYVKPCAPTOINAL 19
Oy :|||:|||:|||:|||:
Db 410 LEPKKVVKPCAPTRLGL 428

RESULT 12

A29619
Vg1 embryonic growth factor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 21-Jul-2000

C;Accession: A29619

R;Weeks: D.L.; Melton, D.A.

Cell 51, 861-867, 1987

A;Title: A maternal mRNA localized to the vegetal hemisphere in Xenopus eggs codes for a

A;Reference number: A29619; MUID:88052889; PMID:3179264

A;Molecule type: mRNA

A;Residues: 1-360 <WEE>

A;Cross-references: GB:M18055; NID:9214179; PIDN:AAA49727.1; PID:g214180

C;Superfamily: inhibin

C;Keywords: growth factor

Query Match 64.0%; Score 71; DB 2; Length 360;
Best Local Similarity 55.0%; Pred. No. 0.0074; Mismatches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 INPETYVKPCAPQNLNS 20
Oy :|||:|||:|||:|||:
Db 315 IEPEDIPPLCCVPTKNSPI 334

RESULT 13

A26158
decapentaplegic protein precursor - fruit fly (*Drosophila melanogaster*)
C;Species: Drosophila melanogaster

C;Accession: A26158
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 16-Apr-1999

R;Padgett, R.W.; St. Johnston, R.D.; Gelbart, W.M.

Nature 325, B1-84, 1987

A;Title: A transcript from a *Drosophila* pattern gene predicts a proprotein homologous to the

A;Reference number: A26158; MUID:87090408; PMID:3467201

A;Accession: A26158

A;Molecule type: mRNA

A;Residues: 1-588 <PAD>

A;Cross-references: GB:M30116; NID:9157291; PID:9157292

C;Genetics:

A;Gene: FLYBase:FBgn0000490

C;Keywords: glycoprotein

F;1-15?domain: signal sequence #status predicted <SIG>
F;1-20,342,377,529?Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 71; DB 2; Length 588;

Best Local Similarity 55.0%; Pred. No. 0.012; Mismatches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 INPETYVKPCAPQNLNS 20
Oy :|||:|||:|||:|||:
Db 543 MNPGKVVKPCAPQNLNSPI 562

RESULT 14

A45056
osteogenic protein 2 precursor - human

N;Alternate names: bone morphogenetic protein 8; OP-2

C;Species: Homo sapiens (man)

C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999

C;Accession: A45056
R;Ozskaynak, E.; Schengelberg, P.N.; Jin, D.F.; Clifford, G.M.; Warren, F.D.; Drier, E.M.

J. Biol. Chem. 267, 25220-25227, 1992

A;Title: Osteogenic protein-2. A new member of the transforming growth factor-beta superfamily

A;Reference number: A45056; MUID:91094231; PMID:1460021

A;Accession: A45056

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-402 <OZK>

A;Cross-references: GB:M97016; NID:9189399; PIDN:AB01360.1; PID:g189390

A;Experimental source: hippocampus

A;Note: sequence extracted from NCBI backbone (NCBIP:120189)

A;Gen: GDB:BMP8; OP-2

A;Cross-references: GDB:136392

C;Superfamily: inhibin

Query Match 63.1%; Score 70; DB 2; Length 402;

Best Local Similarity 60.0%; Pred. No. 0.011; Mismatches 6; Indels 0; Gaps 0;

Matches 12; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 INPETYVKPCAPQNLNS 20
Oy :|||:|||:|||:|||:
Db 357 MKDNANAVPACAPTKSATS 376

RESULT 15

S52408

SPDVRI protein - sea urchin (*Strongylocentrotus purpuratus*)

C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Accession: S52408

R;Ponce, M.R.; Micoli, J.L.; Davidson, E.H.

submitted to the EMBL Data Library, February 1995

A;Description: SPDVRI, a member of the transforming growth factor-beta superfamily expressed in gonads

A;Reference number: S52408

A;Accession: S52408

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-461 <POB>

A;Cross-references: GBL:Z48313; NID:9673496; PID:9673497

C;Superfamily: inhibin

Query Match 63.1%; Score 70; DB 2; Length 461;

Best Local Similarity 55.0%; Pred. No. 0.013; Mismatches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 INPETYVKPCAPQNLNS 20
Oy :|||:|||:|||:|||:
Db 416 MSPSHVQPCAPTKSIT 435

Search completed: October 12, 2004, 09:38:16

Job time : 31 secs

OM protein - protein search, using sw model

Run on: October 12, 2004, 09:02:13 ; Search time 89 Seconds
 Sequence: 1 INPETV2KPCCACTQLNAlS 20
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1017041
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Searched: 1017041 seqs, 315518202 residues

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPREMBL 25;*

1: sp_archeal:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rendon:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_battiriap:*

17: sp_archeap:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	111	100.0	49	6 Q9M2L9	Q9M2L9 canis famili
2	111	100.0	108	6 Q8MJCO	Q8MJCO ovus aries
3	111	100.0	313	13 Q91A03	Q91A03 gallus gallus gallus
4	111	100.0	398	13 Q91B76	Q91B76 gallus gallus gallus
5	108	97.3	141	11 Q88J84	Q88J84 ratus norvegicus
6	108	97.3	306	11 Q9R228	Q9R228 rattus norvegicus
7	108	97.3	424	13 Q9YGH7	Q9YGH7 xenopus laevis
8	102	91.9	432	13 Q9PF99	Q9PF9 brachydanio
9	97	87.4	100	6 Q8MJCI	Q8MJCI ovus aries
10	97	87.4	435	11 Q8BR33	Q8BR33 mus musculus
11	97	87.4	506	11 Q81154	Q81154 rattus norvegicus
12	89	80.2	446	13 Q7ZB88	Q7ZB88 brachydanio
13	87	78.4	453	13 P87373	P87373 gallus gallus
14	87	78.4	454	11 Q8CC80	Q8CC80 mus musculus
15	79	71.2	435	5 Q9U1G4	Q9U1G4 halictis tu
16	79	71.2	178	5 Q25211	Q25211 Junonia coe

ALIGNMENTS

RESULT 1

Q9M2L9 PRELIMINARY; PRT; 49 AA.

ID Q9M2L9
 AC Q9M2L9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Bone morphogenetic protein BMP7 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF172412; AAF89752.1; -.
 RP SOURCE FROM N.A.
 RA Johnson J.A., Breen M., Murphy K.E.;
 RT "Chromosomal Localization of the Genes Encoding Canine Bone Morphogenetic Proteins 4 and 7 (BMP4 and BMP7)." ;
 RT Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 RL CC
 CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF172412; AAF89752.1; -.
 DR HSP; P18075; 1BMP.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PDDOM; PD000357; TGBb; 1.
 DR SMART; SM00204; TGFb; 1.
 FT NON_TER 1
 SQ SEQUENCE 49 AA; 5493 MN; 9AEF2C1B144526EFB CRC64;
 Query Match 100.0%; Score 111; DB 6; Length 49;
 Best Local Similarity 100.0%; Pred. No. 9; 8e-11;
 Matches 20; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 1 INPETV2KPCCACTQLNAlS 20
 4 INPETV2KPCCACTQLNAlS 23

RESULT 2

Q8MJCO

RESULT 3

Q91403 ID Q91403 PRELIMINARY; PRT; 313 AA.

AC Q91403; "TREMBlrel_01, Created"

DT 01-NOV-1996 (TREMBlrel_01, Last sequence update)

DT 01-JUN-2003 (TREMBlrel_24, Last annotation update)

DR Bone morphogenetic Protein-7 (fragment).

OS Ovis aries (Sheep); Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Caprinae; Ovis.

NCBI_TaxID=9440;

[1] SQ SEQUENCE FROM N.A.

RA Souza C.J.H.; Baird D.T.; RT "BMP expression in the sheep ovary." Submitted (May-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF508311; AAC4923..1.; GO: GO:0005576; C:extracellular; IEA. GO; GO:0008151; P:cell growth and/or maintenance; IEA.

DR InterPro; IPR002405; Inhibin_alpha.

DR Pfam; PF00019; TGF-beta_1.

DR PRINTS; PR00669; INHIBINA.

DR PRODOM; PD00357; TGFbeta_1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGFB_BETA_1; 1.

FT NON_TER 108 108 NON-TER 108 AA; 12198 MW; 88516813EA521377 CRC64; SQ SEQUENCE FROM N.A.

Query Match 100.0%; Score 111; DB 13; Length 313; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 INPBTVPKCCAPQNLNIS 20

RESULT 4

Q91876 ID Q91876 PRELIMINARY; PRT; 398 AA.

AC Q91876; "TREMBlrel_15, Created"

DT 01-OCT-2000 (TREMBlrel_15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel_24, Last annotation update)

DR Bone morphogenetic protein 7 (Fragment).

GN BMP7.

OS Gallus gallus (Chicken); OC Bovaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; NCBI_TaxID=9031;

RN DR PRINTS; PR00669; INHIBINA.

RN SEQUENCE FROM N.A.

RC TISSUE_Oviduct; RX MEDLINE=20307867; PubMed=10848589;

RA Monroe D.G.; Jim D.F.; Sanders M.M.; DR "Estrogen Opposes the Apoptotic Effects of Bone Morphogenetic Protein 7 on Tissue Remodeling." Mol. Cell. Biol. 20:4926-4934 (2000).

RT -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF205877; AA34179..1.; HSPB; PI8075; IBM.

DR GO; GO:0008151; C:extracellular; IEA.

DR InterPro; IPR002405; Inhibin_alpha.

DR InterPro; IPR001839; TGFB.

DR Pfam; PF00019; TGF-beta_1.

DR Pfam; PF00688; TGFB_propeptide; 1.

DR PRINTS; PR00669; INHIBINA.

DR PRODOM; PD00357; TGFbeta_1.

SMART; SM00204; TGFB; 1.

PROSITE; PS00250; TGFB_BETA_1; 1.

FT NON_TER 1 1 SQ SEQUENCE 398 AA; 45459 MW; 9C3F625299DD0C37 CRC64;

Query Match 100.0%; Score 111; DB 13; Length 398; Best Local Similarity 100.0%; Pred. No. 8e-10; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 353 INPBTVPKCCAPQNLNIS 372

RESULT 5

Q98684 ID Q98684 PRELIMINARY; PRT; 141 AA.

AC Q98684; "TREMBlrel_08, Created"

DT 01-NOV-1998 (TREMBlrel_08, Last sequence update)

DT 01-NOV-1998 (TREMBlrel_08, Last sequence update)

DT 01-JUN-2003 (TREMBlrel_24, Last annotation update)

DE Bone morphogenetic protein-7 (Fragment).

OS Rattus norvegicus (Rat).

DR PRINTS; PR00669; INHIBINA.

DR PRODOM; PD000357; TGFB; 1.

DR SMART; SM00204; TGFB; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

FT NON_TER 1 1 SQ SEQUENCE 313 AA; 35816 MW; COA3739197DBAC8F CRC64;

Query Match 100.0%; Score 111; DB 13; Length 313; Best Local Similarity 100.0%; Pred. No. 6.3e-10; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 268 INPBTVPKCCAPQNLNIS 287

DR	PROSITE; PS02550; TGF_BETA_1; 1.
KW	HYPOTHETICAL protein; Signal.
SIGNAL	9 29
CHAIN	285 424
SEQUENCE	424 AA; 48917 MW; C4638CTD3D0A1DE4 CRC64;
QY	1 INPETPKPCCAPTOINAI S 20
RESULT	8
ID	Q9PTF9
AC	Q9PTF9;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
RT	"Essential role of Bmp7 (snailhouse) and its prodomain in dorsoventral patterning of the zebrafish embryo"; Development 0-0 (2000) -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DE	Bone morphogenetic protein 7.
GN	BMP7; OR BMP7.
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=TL;
RA	Dick A., Hild M., Bauer H., Imai Y., Maifeld H., Schier A.F., Talbot W.S., Bouwmeester T., Hammerschmidt M.; prodomain in dorsoventral patterning of the zebrafish embryo"; Development 0-0 (2000) -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
RT	"Essential role of Bmp7 (snailhouse) and its prodomain in dorsoventral patterning of the zebrafish embryo"; Development 0-0 (2000) -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
RU	Talbot W.S., Bouwmeester T., Hammerschmidt M.; prodomain in dorsoventral patterning of the zebrafish embryo"; Development 0-0 (2000) -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR	EMLB; AF201379; AAFT7558.1; -.
DR	HSSP; P18075; TGFb; 1.
DR	ZFIN; ZDB-GENE:000208-25; bmp7.
DR	InterPro; IPR01839; TGFb.
DR	InterPro; IPR01111; TGFb_N.
DR	Pfam; PF00019; TGFb_propeptide; 1.
DR	ProDom; PD00357; TGFb; 1.
DR	SMART; SM00204; TGFb; 1.
DR	PROSITE; PS00250; TGF_BETA_1; 1.
DR	SOQUENCE; 432 AA; 48923 MW; C982AF80B1652156 CRC64;
QY	1 INPETVPKPCAPTOINAI S 20
Db	387 INPETVPKPCAPTOINAI S 406
RESULT	9
Q8WJCI	PRELIMINARY; PRT; 100 AA.
AC	Q8WJCI;
DT	01-OCT-2002 (TREMBLrel. 22, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Bone morphogenetic protein 6 (Fragment).
OS	Ovis aries (Sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
OC	NCBI_TaxID=9940;
[1]	
QY	1 INPENVPKPCAPTOINAI S 20
RESULT	11
Q81S4	PRELIMINARY; PRT; 506 AA.
ID	Q81S4
AC	Q81S4;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
QY	1 INPENVPKPCAPTOINAI S 20
RESULT	17
Q81S4	PRELIMINARY; PRT; 435 AA.
ID	Q81S4
AC	Q81S4;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
QY	1 INPENVPKPCAPTOINAI S 20
RESULT	11
Q81S4	PRELIMINARY; PRT; 506 AA.
ID	Q81S4
AC	Q81S4;
DT	01-JUN-2003 (TREMBLrel. 24, Created)

01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bone morphogenetic protein 6.
 GN BMP6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1] NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A.
 RC STRAIN_Sprague Dawley;
 RA Li H.; Li J.; Pittman D.D.; Amalfitano A.; Hankins G.R.; Heilm G.A.;
 RT "An Immunological Study of BMP6 Adenoviral Gene Therapy.";
 RL Submitted (Nov-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY184240; AAQ25744.1; -.
 DR InterPro; IPR001833; TGFB.
 DR IPR001111; TGFB_N.
 DR Pfam; PF00019; TGF-beta_1.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR Prodrom; PDD00357; TGFB; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE: 506 AA; 56222 MW; 703D077D7B94416C CRC64;
 Query Match 87.4%; Score 97; DB 11; Length 506;
 Best Local Similarity 85.0%; Pred. No. 28-07;
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 INPTEVVKPCCAPTQNAIS 20
 Db 461 MNPEYYVKPCCAPTQNAIS 480

RESULT 12
 Q7T288 PRELIMINARY; PRT; 446 AA.
 ID Q7T288
 AC 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DR Hypothetical protein.
 DS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
 RA Klausner R.D.; Collins F.S.; Wagner L.; Shevchenko C.M.; Schuler G.D.,
 RA Altschul S.F.; Zeeberg B.; Butow K.H.; Scheffer C.P.; Bhat N.K.,
 RA Hopkins R.P.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.,
 RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
 RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.,
 RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.,
 RA Raha S.S.; Logueano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.,
 RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.,
 RA Richards S.; Worley K.C.; Haile S.; Garcia A.M.; Gavriloff S.W.,
 RA Villalon D.K.; Muñoz D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.; Hulyk S.W.,
 RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.,
 RA Whiting M.; Madan A.; Young A.C.; Shvchenko Y.; Bouffard G.G.,
 RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickon M.C.,
 RA Rodriguez A.C.; Grimeswood J.; Schmutz J.; Myers R.N.; Butterfield Y.S.,
 RA Krzywinski M.I.; Skalska U.; Smalius D.E.; Schniechen A.; Schein J.E.,
 RA Jones S.J.; Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RA proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RC SEQUENCE FROM N.A.
 RN TISSUE=Embryo;

RESULT 13
 P87373 PRELIMINARY; PRT; 453 AA.
 ID P87373
 AC 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DR 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE BMP5.
 GN Gallus gallus (Chicken).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=97000882; PubMed=8615925;
 RA Oh S.H.; Johnson R.; Wu D.K.;
 RT "Differential expression of bone morphogenetic proteins in the
 developing vestibular and auditory sensory organs.";
 RT J. Neurosci. 16:6663-6675 (1996).
 RL -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; S83278; AAB9514.1; -.
 DR HSSP; PI8075; IBM.
 DR InterPro; IPR002400; GF_cysknott.
 DR InterPro; IPR001839; TGFB.
 DR InterPro; IPR001111; TGFB_N.
 DR Pfam; PF00019; TGF-beta_1.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR Prodrom; PDD00357; TGFB.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR SEQUENCE: 453 AA; 51628 MW; AB946FR878BF32B2 CRC64;
 Query Match 78.4%; Score 87; DB 13; Length 453;
 Best Local Similarity 83.3%; Pred. No. 75e-06;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 3 PETVVKPCCAPTQNAIS 20
 Db 410 PDHVVKPCCAPTQNAIS 427

RESULT 14
 Q8CCB0 PRELIMINARY; PRT; 454 AA.
 ID Q8CCB0
 AC 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DR Bone morphogenetic protein 5.
 GN BMP5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] TISSUE=Embryo;

Search completed: October 12, 2004, 09:37:40
 Job time : 91 secs

RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=2354683; PubMed=12466851;
 RA The FANTOM Consortium,
 the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK03362; BAC8247.1; -.
 DR MGI; MGI:8911; Bmp5.
 DR GO; GO:0007389; P:pattern specification; IMP.
 DR GO; GO:001501; P:skeletal development; IMP.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGFB.
 DR Pfam; PF00019; TGF-beta; I.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR PRINTS; PRO0438; GFCYSKNOT.
 DR PRODOM; PD000357; TGFB; 1.
 DR SMART; SM0204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 454 AA; 51727 MW; 722EA34FF25D63A0 CRC64;
 Query Match 78.4%; Score 87; DB 11; Length 454;
 Best Local Similarity 83.3%; Pred. No. 7.5e-06;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 PETWPKPCCAPQNLNAIS 20
 OX 411 PDAVPKKCCAPQNLNAIS 428
 Db

RESULT 15

Q91G4 PRELIMINARY; PRT; 87 AA.
 ID Q91G4
 AC
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)
 DB BMP2/4 protein (Fragment).
 GN Haliothis tuberculata.
 OC Bivalvia; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Venerida; Bivalvia; Haliozoidea; Haliotidae; Haliotis.
 OX NCBI_TaxID=36103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mantle;
 RX MEDLINE=21261484; PubMed=11368950;
 RA Lelong C., Mathieu M., Favre P.;
 RT "Identification of new bone morphogenetic protein-related members in
 invertebrates";
 RL Biochimie 83:423-426 (2001).
 CC -- SIMILARITY: BELONGS TO THE TGF-BBTA FAMILY.
 DR EMBL; AU251923; CAB61656.1; -.
 DR HSPB; P12643; 3BMP.
 DR InterPro; IPR001839; TGFB.
 DR Pfam; PF00019; TGF-beta; I.
 DR PRODOM; PD000357; TGFB; 1.
 DR SMART; SM0204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 FT NON_TER 1
 FT NON_TER 87
 SEQUENCE 87 AA; 9565 MW; 705965FCBCDBFFE6 CRC64;
 Query Match 71.2%; Score 79; DB 5; Length 87;
 Best Local Similarity 65.0%; Pred. No. 2.9e-05;
 Matches 13; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 1 INPFTVPKPCCAPQNLNAIS 20
 OX 44 VNFSAVPKKCCAPQNLNAIS 63
 Db

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 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimeswood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E.,
 RA Schmerch A., Schain J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL PROC.
 CC osteoinductive factor responsible for the phenomenon of epithelial
 CC osteogenesis. Plays a role in calcium regulation and bone
 CC homeostasis.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; X56906; CAA40222.1; -.
 DR EMBL; BC010711; AAH10711.1; -.
 DR HSSP; P18075; 1BMP.
 DR MGI; MGI:03302; Bmp7.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:007411; P:axon guidance; IDA.
 DR GO; GO:003887; P:organogenesis; IMP.
 DR GO; GO:007389; P:pattern specification; IMP.
 DR GO; GO:007435; P:salivary gland morphogenesis; IMP.
 DR InterPro; IPR01839; TGFb.
 DR InterPro; IPR0111; TGFb.
 DR Pfam; PF00019; TGFb-beta; 1.
 DR Pfam; PF0088; TGFb; propeptide; 1.
 DR ProDom; PDD00357; TGB; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF-BETA_1; 1.
 DR Signal; Growth Factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 29 POTENTIAL.
 FT PROPEP 30 291 POTENTIAL.
 FT CHAIN 292 430 BONE MORPHOGENETIC PROTEIN 7.
 FT DISULFID 329 395 BY SIMILARITY.
 FT DISULFID 358 427 BY SIMILARITY.
 PT DISULFID 362 429 BY SIMILARITY.
 PT DISULFID 394 394 INTERCHAIN (BY SIMILARITY).
 PT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 371 371 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CONFLICT 167 167 A -> R (IN REF. 1).
 SQ SBQENSE 430 AA; 49198 MW; 464F36D5D2E54041 CRC64;

Query Match 97.3%; Score 108; DB 1; Length 430;
 Best Local Similarity 95.0%; Pred. No. 8e-09; Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETVPKCCAPTOQNAIS 20
 Db 385 INPDIVPKPCAPTOQNAIS 404

RESULT 3

BMP7_XENLA
 ID BMP7_XENLA STANDARD; PRT; 426 AA.
 AC P30886; Q9I645; 01-JUL-1993 (Rel. 25, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 7 precursor (BMP-7) (osseogenic protein 1)

DB (OP-1) (XKMP7).
 GN BMP7.
 OS Xenopus laevis (African clawed frog).
 OC Buka-Yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopidae;
 OC Xenopus.
 RN [1] Nishimatsu S., Suzuki A., Shioya A., Murakami K., Ueno N.;
 RN "Genes for bone morphogenetic proteins are differentially transcribed
 RN in early amphibian embryos.", Submitted (DSC-1995) to the EMBL/Genbank/DBJ databases.
 RN [2] Hawley S.H.B., Wunderlich-Stapleton K., Hashimoto C.,
 RN Laurent M.N., Watabe T., Blumberg B.W., Cho K.W.Y.;
 RN Biochem. Biophys. Res. Commun. 186:1487-1495 (1992).
 RP SEQUENCE FROM N.A.
 RA MEDLINE=92378616; PubMed=1510575;
 RA Nishimatsu S., Suzuki A., Shioya A., Murakami K., Ueno N.;
 RA "Genes for bone morphogenetic proteins are differentially transcribed
 RA in early amphibian embryos.", Submitted (DSC-1995) to the EMBL/Genbank/DBJ databases.
 RA -!- FUNCTION: Induces cartilage and bone formation. May be the
 RA osteoinductive factor responsible for the phenomenon of epithelial
 RA osteogenesis. Plays a role in calcium regulation and bone
 RA homeostasis.
 RA -!- SUBUNIT: Homodimer; disulfide-linked.
 RA -!- SIMILARITY: Belongs to the TGF-beta family.

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CC EMBL; X56906; CAA40221.1; -.
 CC DR EMBL; BC010711; AAH10711.1; -.
 CC DR HSSP; P18075; 1BMP.
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 CC or send an email to license@isb-sib.ch).

CC EMBL; X56906; CAA40221.1; -.
 CC DR EMBL; BC010711; AAH10711.1; -.
 CC DR HSSP; P18075; 1BMP.
 DR InterPro; IPR01839; TGFb.
 DR InterPro; IPR0111; TGFbeta.
 DR InterPro; IPR0019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb; propeptide; 1.
 DR ProDom; PDD00357; TGFb; 1.
 DR SMART; SM00204; TGB; 1.
 DR PROSITE; PS00250; TGF-BETA_1; 1.
 DR Signal; Growth Factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 282 POTENTIAL.
 FT CHAIN 283 426 BONE MORPHOGENETIC PROTEIN 7.
 FT DISULFID 325 391 BY SIMILARITY.
 FT DISULFID 354 423 BY SIMILARITY.
 FT DISULFID 358 425 BY SIMILARITY.
 PT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).
 PT CARBOHYD 397 377 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CONFLICT 317 319 KRR -> NWV (IN REF. 2).
 PT CONFLICT 355 355 D -> E (IN REF. 2).
 SQ SEQUENCE 426 AA; 49565 MW; 6401D51IAC97117 CRC64;

Query Match 96.4%; Score 107; DB 1; Length 426;
 Best Local Similarity 95.0%; Pred. No. 1.e-08; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INPETVPKCCAPTOQNAIS 20
 Db 381 INPDIVPKPCAPTOQNAIS 400

RESULT 4

BMP6_RAT
 ID BMP6_RAT STANDARD; PRT; 207 AA.

PT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 451 451 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CONFLICT 73 73 K. -> M (IN REF. 3).
 PT CONFLICT 75 75 E -> K (IN REF. 3).
 FT CONFLICT 86 86 L -> P (IN REF. 3).
 SQ SEQUENCE 510 AA; 56431 MW; 910B68531289FC0D2 CRC64;
 Query Match 87.4%; Score 97; DB 1; Length 510;
 Best Local Similarity 85.0%; Pred. No. 4.2e-07; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 17; Conservative 2; MisMatches 1; Indels 0; Gaps 0;
 Qy 1 INPETYVKPCAPQNLNS 20
 Db 465 MNPEYVVPKPCAPTKLNNS 484

RESULT 6
 BMP6_HUMAN STANDARD; PRT; 513 AA.
 AC P22004;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 6 precursor (BMP-6).
 GN BMP6 OR VGR.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=910B88608; PubMed=2263336;
 RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
 RA Wang E.A., Wozney J.M.;
 RT Identification of transforming growth factor beta family members
 present in bone-inductive protein purified from bovine bone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9434-9447 (1990).
 CC -- FUNCTION: Induces cartilage and bone formation.
 CC -- SIMILARITY: Belongs to the TGF-beta family.
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 or send an email to license@isb-sib.ch).
 CC -----
 EMBL; M60315; AAA36737.1; -.
 DR HSSP; P1075; 1BMP.
 DR Genew; HGNC:1073; BMP6.
 DR MIM: 112666; -. P: skeletal development; TAS.
 DR GO:001501; P: skeletal development; TAS.
 DR InterPro; IPR001839; TGFB.
 DR InterPro; IPR00111; TGFB_N.
 DR Pfam; PF00019; TGF-beta_1.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR Prodrom; PD000357; TGFB; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein. Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 381 POTENTIAL.
 FT CHAIN 382 513 BONE MORPHOGENETIC PROTEIN 6.
 FT DISULFID 412 478 BY SIMILARITY.
 FT DISULFID 441 510 BY SIMILARITY.
 FT DISULFID 445 512 BY SIMILARITY.
 FT DISULFID 477 477 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 513 AA; 57225 MW; 3F1915B36149278 CRC4;
 Query Match 87.4%; Score 97; DB 1; Length 513;
 Best Local Similarity 85.0%; Pred. No. 4.2e-07; 2; Mismatches 1; Indels 0; Gaps 0;
 Matches 17; Conservative 2; MisMatches 1; Indels 0; Gaps 0;
 Qy 1 INPETYVKPCAPQNLNS 20
 Db 468 MNPEYVVPKPCAPTKLNNS 487

RESULT 7
 BMP5_MOUSE STANDARD; PRT; 452 AA.
 ID BMP5_MOUSE
 AC P49031;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 5 precursor (BMP-5).
 GN BMP5 OR BMP-5.
 CS Mus musculus (Mouse).
 CC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10909;
 RN [1]
 RP SEQENCE FROM N.A.
 RC STRAIN=C57BL/KW;
 RX MEDLINE=95046894; PubMed=7958439;
 RA King J.A., Marker P.C., Kingsley D.M.;
 RT "BMP5 and the molecular, skeletal, and soft-tissue alterations in
 short ear mice." Dev. Biol. 166:112-122(1994).
 RL Dev. Biol. 166:112-122(1994).
 CC --!- FUNCTION: Induces cartilage and bone formation.
 CC --!- SUBMIT: Homodimer; disulfide-linked (By similarity).
 CC --!- SIMILARITY: Belongs to the TGF-beta family.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M41145; AAC64612.1; -.
 DR PIR; I43542; I49342.
 DR HSSP; P18075; 1BMP.
 DR MGD; MGI:88181; Bmp5.
 DR GO; GO:0007369; P:pattern specification; IMP.
 DR GO; GO:0001501; P:skeletal development; IMP.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGFB.
 DR InterPro; IPR00111; TGFB_N.
 DR Pfam; PF00019; TGF-beta; T.
 DR Pfam; PF00688; TGFB_propeptide; 1.
 DR Pfam; PF00038; GFCYSNOT.
 DR Prodrom; PD000357; TGFB; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Glycoprotein. Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW SIGNAL 1 25 POTENTIAL.
 FT PROPEP 26 320 BONE MORPHOGENETIC PROTEIN 6.
 FT CHAIN 321 452 BY SIMILARITY.
 FT DISULFID 351 417 BY SIMILARITY.
 FT DISULFID 380 449 BY SIMILARITY.
 FT DISULFID 384 451 BY SIMILARITY.
 FT DISULFID 416 416 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	343	343	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC
FT	CARBONYD	393	393	N-LINKED (GLCNAC. . .) (POTENTIAL).	CC
SQ	SEQUENCE	452 AA;	51511 MW;	AD9521EC9A7BDS CRG64;	DR
Query Match	Best Local Similarity	78.4%	Score	87; DB 1; Length 452;	DR
Matches	15; Conservative	83.3%; Pred.	No.	1.2e-05; 1; Indels 0; Gaps 0;	DR
QY	3 PETVPKPCAPTOINAI	20	Db	409 PDHVPKPCAPTKNAIS 426	DR
RESULT 8	BMP5_HUMAN	STANDARD;	PRT;	454 AA.	DR
ID	P22003; Q9H547; Q9TNM5;				DR
AC	01-AUG-1991 (Rel. 19, Last sequence update)				DR
DT	15-MAR-2004 (Rel. 43, Last annotation update)				DR
DE	Bone morphogenetic protein 5 precursor (BMP-5).				DR
GN	Homo sapiens (Human).				DR
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				DR
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				DR
OX	NCBI_TaxID=9606;				DR
RN	[1]				DR
RP	SEQUENCE FROM N.A.				DR
RC	TISSUE=Bone;				DR
RX	MEDLINE:91086608; PubMed=2263636;				DR
RA	Colleste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,				DR
RA	Wang B.A., Wozney J.M.;				DR
RT	"Identification of transforming growth factor beta family members present in bone-inductive protein purified from bovine bone.";				DR
RT	Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).				DR
RL	[2]				DR
RN	SEQUENCE FROM N.A.				DR
RA	Bates K., Tracey A.;				DR
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				DR
RN	[3]				DR
RP	SEQUENCE FROM N.A.				DR
RC	TISSUE=Lung, and Spleen;				DR
RX	MEDLINE:22382257; PubMed=12477937;				DR
RA	Straubinger R.D., Feinsold E.A., Grouse L.H., Derge J.G.,				DR
RA	Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schuler G.D.,				DR
RA	Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blatt N.K.,				DR
RA	Hopkins R.P., Jorcan H., Moore T., Max S.I., Wang J., Hsieh F.,				DR
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				DR
RA	Stupleton M., Soares M.B., Donaldson M.F., Casavant T.L., Scheetz T.E.,				DR
RA	Brownstein M.J., Usdin T.B., Toshinuki S., Carninci P., Prange C.,				DR
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,				DR
RA	Osakai S.A., McEwan F.J., McFern K.J., Malek J.A., Gunaratne P.H.,				DR
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				DR
RA	Villalon D.K., Muzy D.M., Sodersten E.J., Liu X., Gibbs R.A.,				DR
RA	Fahey J., Helton M., Madan A., Rodrigues S., Sanchez A.,				DR
RA	Whiting M., Madan A., Young A.C., Shevchenko T., Bouffard G.G.,				DR
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				DR
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				DR
RA	Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,				DR
RA	Gehrmrich A., Schein J.E., Jones S.J.M., Matra M.A.,				DR
RT	"Gehrmrich and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."				DR
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				DR
CC	-- FUNCTION: Induces cartilage and bone formation.				DR
CC	-- SUBUNIT: Homodimer; disulfide-linked (By similarity).				DR
CC	-- TISSUE SPECIFICITY: Expressed in the lung and liver.				DR
CC	-- SIMILARITY: Belongs to the TGF-beta family.				DR
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				DR
CC	-----				DR
CC	EMBL; M60314; AAA36736.1; --.				DR
CC	EMBL; AL133178; CAC12765.1; --.				DR
CC	EMBL; BC02195; AAH27958.1; --.				DR
CC	EMBL; A39263; BM4US.				DR
CC	PTR; A39265; BMP5.				DR
CC	Gene; HGNC:1072; BMP5.				DR
CC	MIM; 112265; --.				DR
CC	GO; GO:0001501; P:skeletal development; NAS.				DR
CC	InterPro; IPRO02400; GF_cysknot.				DR
CC	InterPro; IPR001839; TGFB.				DR
CC	InterPro; IPR001111; TGFB_N.				DR
CC	PFam; PF00019; TGFB_Propeptide_1.				DR
CC	PRINTS; PRO0438; GFCSKNOT.				DR
CC	PRINTS; PRO00357; TGFB_1.				DR
CC	SMART; SM0204; TGFB_1.				DR
CC	PROSITE; PRO0250; TGFB_BETA_1.				DR
CC	Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis; Glycoprotein.				DR
CC	KW				DR
CC	PT SIGNAL 1 30 POTENTIAL.				DR
CC	PT PROPEP 31 322 BONE MORPHOGENETIC PROTEIN 5.				DR
CC	PT CHAIN 323 454 BY SIMILARITY.				DR
CC	PT DISULFID 335 419 BY SIMILARITY.				DR
CC	PT DISULFID 382 451 BY SIMILARITY.				DR
CC	PT DISULFID 386 453 INTERCHAIN_BY_SIMILARITY.				DR
CC	PT DISULFID 418 211 N-LINKED (GLCNAC. . .) (POTENTIAL).				DR
CC	PT CARBOHYD 211 327 N-LINKED (GLCNAC. . .) (POTENTIAL).				DR
CC	PT CARBOHYD 327 345 N-LINKED (GLCNAC. . .) (POTENTIAL).				DR
CC	PT CARBOHYD 345 395 N-LINKED (GLCNAC. . .) (POTENTIAL).				DR
CC	SO SEQUENCE 454 AA; 51736 MW; 631277413CCC22BE CRG64;				DR
Query Match	Best Local Similarity	78.4%	Score	87; DB 1; Length 454;	CC
Matches	15; Conservative	83.3%; Pred.	No.	1.2e-05; 1; Indels 0; Gaps 0;	CC
QY	3 PETVPKPCAPTOINAI	20	Db	411 PDHVPKPCAPTKNAIS 428	CC
RESULT 9	60A_DROVI	STANDARD;	PRT;	436 AA.	CC
ID	60A_DROVI				CC
AC	Q24735;				CC
DT	01-NOV-1997 (Rel. 35, Created)				CC
DT	01-NOV-1997 (Rel. 35, Last sequence update)				CC
DT	15-OCT-2001 (Rel. 40, Last annotation update)				CC
DE	60A protein precursor (Glass bottom boat protein).				CC
DN	GBB OR 60A OR TGFB-60A.				CC
OS	Drosophila virilis (Fruit fly).				CC
OC	Eukaryota; Metazoa; Athrora; Dipaea; Brachycera; Muscomorpha; Ocularia; Ephydriidae; Drosophilidae; Drosophila.				CC
OC	NCI_TaxID=7244;				CC
RN	[1]				CC
RP	SEQUENCE FROM N.A.				CC
RX	MEDLINE=96105349; PubMed=8688461;				CC
RX	Du W., Doctor J.S.;				CC
RT	"Isolation and sequence of the Drosophila virilis 60 A gene, a transforming growth factor-beta superfamily member related to vertebrate bone morphogenetic proteins."				CC
RT	Verheyen, C., Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ocularia; Ephydriidae; Drosophilidae; Drosophila.				CC
RL	Biochim. Biophys. Acta 1307:273-279(1996).				CC
CC	-- SUBUNIT: Homodimer; disulfide-linked (By similarity).				CC
CC	-- SIMILARITY: Belongs to the TGF-beta family.				CC
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute.				CC
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				CC
CC	-----				CC

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CC STRAIN=Birkeley;
 CC MEDLINE=20196006; PubMed=10731132;
 RX RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 CC or send an email to license@isb-sib.ch.
 CC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 DR Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 DR HSSP; P18075; IBMPC.
 DR FlyBase; FBgn0015681; Dvir\gbb.
 DR InterPro; IPR002400; GF_cysknott.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFbN.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00588; TGFb_propeptide; 1.
 DR PRINTS; PRO0438; GF_CYSNOT.
 DR PRODOM; PD000357; TGFb; 1.
 DR SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 27
 FT PROPEP 28 317
 FT CHAIN 318 436
 FT DISULFID 335 401
 FT DISULFID 364 433
 FT DISULFID 435 400
 FT CARBOHYD 102 102
 FT CARBOHYD 114 114
 FT CARBOHYD 217 217
 FT CARBOHYD 229 229
 FT CARBOHYD 377 377
 FT SEQUENCE 436 AA; 49999 MW; C74BAE58796692 CRC64;
 Query Match 69.4%; Score 77; DB 1; Length 436;
 Best Local Similarity 63.2%; Pred. No. 0.00035;
 Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 INPBTVPKCCAPQTLNAT 19
 OC :|:|||:|||:|||:
 Db 391 LEPKRNPKEPCAPTRIGAL 409

RESULT 10

60A_DROME

ID_ 60A_DROME STANDARD; PRT; 455 AA.

AC P27091; Q9W14;

DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE rel. 42, last annotation update)

GN BOR 60A OR TGBB-60A OR CG5562.

OS Drosophila melanogaster (Fruit fly).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.

OC NCBI_TAXID=7227;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=92021021; PubMed=1924384;

RA Whartman K.A., Thomsen G.H., Gelbart W.M.;
 RT "Drosophila 60A gene, another transforming growth factor beta family member, is closely related to human bone morphogenetic proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:9214-9218(1991).
 RN [2] SEQUENCE FROM N.A.

RX MEDLINE=92280120; PubMed=1601181;
 RX MEDLINE=92280120; PubMed=1601181;
 RA Doctor J.S., Jackson P.D., Rashka K.E., Visalli M., Hoffmann F.M.;
 RT "Sequence, biochemical characterization, and developmental expression of a new member of the TGF-beta superfamily in Drosophila melanogaster.";
 RT Dev. Biol. 151:491-505(1992).
 RN [3] SEQUENCE FROM N.A.

CC STRAIN=Birkeley;
 CC MEDLINE=20196006; PubMed=10731132;
 RX RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 CC Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 CC or send an email to license@isb-sib.ch.
 CC Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 DR Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 DR HSSP; P18075; IBMPC.
 DR FlyBase; FBgn0015681; Dvir\gbb.
 DR InterPro; IPR002400; GF_cysknott.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFbN.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 DR Pfam; PF00588; TGFb_propeptide; 1.
 DR PRINTS; PRO0438; GF_CYSNOT.
 DR PRODOM; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 36

FT PROPEP 37 335 POTENTIAL.
 FT CHAIN 336 455 60A PROTEIN.
 FT DISULFID 354 420 BY SIMILARITY.
 FT DISULFID 383 452 BY SIMILARITY.
 FT DISULFID 387 454 BY SIMILARITY.
 FT DISULFID 419 419 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 250 250 BONE MORPHOGENETIC PROTEIN 8A.
 FT CARBOHYD 396 396 BY SIMILARITY.
 SQ 455 AA; 51687 MW; CBFAT35556341F94 CRC64;
 SQ 69.4%; Score 77; DB 1; Length 455; Best Local Similarity 63.2%; Pred. No. 0.00036; Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 INPBETVPKCCAPQNLAI 19
 Db 410 LEPKRVPKCCAPPRIGAL 428
 RESULT 11
 BM8A_MOUSE STANDARD; PRT; 399 AA.
 ID_BM8A_MOUSE AC P34821; 01-FEB-1994 (Rel. 28, Created)
 DT 15-MAR-2004 (Rel. 28, Last sequence update)
 DE Bone morphogenetic protein 8A precursor (BMP-8A) (Osteogenic protein 2) (OP-2).
 GN BMP8 OR BMP8 OR BMP-8.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TAXID=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE:93094231; PubMed=1460021;
 RA Ozkaynak E., Schneegleiberg P.N.J., Jin D.F., Clifford G.M., Warren F.D., Drier E.A., Oppermann H.;
 RT factor-beta superfamily expressed early in embryogenesis.;
 RL J. Biol. Chem. 267:25220-25227(1992).
 CC -!- FUNCTION: Induces cartilage and bone formation. May be the osteoinductive factor responsible for the phenomenon of epithelial-mesenchymal transition. Plays a role in calcium regulation and bone homeostasis. (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- DEVELOPMENTAL STAGE: EXTENSIVE EXPRESSION FOUND IN 8-DAY EMBRYOS, FELL DRASITICALLY IN 10-DAY EMBRYOS AND VIRTUALLY ABSENT IN 17-DAY EMBRYOS.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
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 CC -!- EMBL; M97017; AAB01365. 1; -.
 DR HSSP; P18075; 1BMP.
 DR MGD; MGT:104515; Bmp8a.
 DR GO; GO:0007283; P-spermatogenesis; IMP.
 DR InterPro; IPR02400; GF_Cysknob.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR01111; TGBb_N.
 DR Pfam; PF00019; TGF-beta_1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PRO0358; GFCYSKNOT.
 DR PRODOM; PD000537; TGFb; 1.
 DR SMART; SM00204; TGFB; 1; TGF_BETA_1; 1.
 DR PROSINE; PS00250; TGF_BETA_1; 1.
 KW Signal; Growth factor; Cytokine; Osteogenesis; Chondrogenesis;
 KW Glycoprotein.
 FT SIGNAL 1 19 POTENTIAL.
 FT PROPEP 20 260 POTENTIAL.
 FT CHAIN 261 399 BY SIMILARITY.
 FT DISULFID 298 364 BY SIMILARITY.
 FT DISULFID 327 396 BY SIMILARITY.
 FT DISULFID 331 398 BY SIMILARITY.
 FT DISULFID 363 363 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ 399 AA; 44764 MW; B7FB32D6125E40C CRC64;
 SQ 64.9%; Score 72; DB 1; Length 399; Best Local Similarity 60.0%; Matches 12; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 INPBETVPKCCAPQNLAI 20
 Db 354 MKPDVVPKCCAPTKLSAT 373
 RESULT 12
 DECA_DROPS STANDARD; PRT; 621 AA.
 ID_DECA_DROPS AC P31699; 01-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Decapentaplegic protein precursor (DPP-C protein).
 GN DPP.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Embryodea; Drosophilidae; Drosophila.
 OC NCBI_TAXID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:97225212; PubMed=9071565;
 RA Newfeld S.J., Padgett R.W., Finlayley S.D., Richter B.G., Sanicola M., de Cuevas M., Gelbart W.M.; "Molecular evolution at the decapentaplegic locus in Drosophila.", Genetics 145:373-309 (1997).
 RT -!- FUNCTION: ACTS AS AN EXTRACELLULAR MORPHOGEN TO ESTABLISH AT LEAST TWO CELLULAR RESPONSE THRESHOLDS WITHIN THE DORSAL HALF OF THE DROSOPHILA EMBRYO. REQUIRED FOR THE PROPER DEVELOPMENT OF THE EMERGENT DORSAL HYPODERM, FOR VIABILITY OF LARVAE AND FOR CELL VIABILITY OF THE EPITHELIAL CELLS IN THE IMAGINAL DISKS. ACTS TOGETHER WITH SCW (BY SIMILARITY).
 CC -!- SUBUNIT: HETEROODIMERS OF SCW/DPP ARE THE ACTIVE SUBUNIT, DPP/DPP HOMODIMERS ELICIT A BASAL RESPONSE AND SCW/SCW HOMODIMERS ALONE ARE INEFFECTIVE IN SPECIFYING A DORSAL PATTERN (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: Expressed in the imaginal discs associated with establishment of the proximal-distal axis of the appendages, and midgut mesoderm (By similarity).
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
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 CC -!- EMBL; U63856; AAC7553.1; -.
 DR HSSP; P12643; 3BMP.
 DR Pfam; PF00019; TGF-beta_1.
 DR MGD; MGT:104515; Bmp8a.
 DR GO; GO:0007283; P-spermatogenesis; IMP.
 DR InterPro; IPR02400; GF_Cysknob.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR01111; TGBb_N.
 DR InterPro; IPRT00019; TGF-beta_1.
 DR InterPro; IPR02400; Inhibin_alpha.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR01111; TGFb_N.

DR Pfam; P00019; TGF-beta; 1.
 DR Pfam; PF0688; TGFb_propeptide; 1.
 DR PRINTS; PRO0669; INHIBINA.
 DR PRODom; PD00357; TGFb; 1.
 DR SMART; SM00204; TGF-BETA_1; 1.
 DR PROSITE; PS00250; TGF BETA_1; 1.
 KW Growth factor; Developmental protein; Differentiation; Glycoprotein;
 KW Signal.
 FT SIGNAL 1 15 POTENTIAL.
 FT PROPEP 16 479 BY SIMILARITY.
 FT CHAIN 480 621 BY DECAPEPTIDE.
 FT DISULFID 520 586 BY SIMILARITY.
 FT DISULFID 549 618 BY SIMILARITY.
 FT DISULFID 553 620 BY SIMILARITY.
 FT DISULFID 585 585 BY SIMILARITY.
 FT DOMAIN 45 57 BY POLY-ALA.
 FT DOMAIN 88 92 BY POLY-ASN.
 FT DOMAIN 95 104 BY POLY-ASN.
 FT DOMAIN 163 173 BY POLY-GIN.
 FT CARBOHYD 483 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 365 365 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ 621 AA; 69038 MW; 3FD7141FB5509651 CRC64;

Query Match Score 72; DB 1; Length 621;
 Best Local Similarity 55.0%; Pred. No. 0.0026; Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0; Signal 1 15 POTENTIAL.

Qy 1 INPETYVKPCAPQTLNAIS 20
 Db 576 LNPQKVPKACVCPQTQLSVA 595

RESULT 13

DVR1_XENLA STANDARD; PRT; 360 AA.
 ID _DVR1_XENLA STANDARD; PRT; 360 AA.
 AC P09534;
 DT 01-MAR-1989 (Rel. 10; Created)
 DT 01-JUN-1994 (Rel. 29; Last annotation update)
 DE DVR-1 protein precursor (Vegetal hemisphere Vg1 protein) (VG-1).
 OS Xenopus laevis (African clawed frog).
 OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Xenopidae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Xenopidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=88052889; PubMed=3479264;
 RA Weeks D.L., Melton D.A.;
 RT "A maternal mRNA localized to the vegetal hemisphere in *Xenopus* eggs codes for a growth factor related to TGF-beta.";
 RL Cell 51:861-867(1987).
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=8905504; PubMed=2519312;
 RA Dale L., Matthews G., Tobe L., Colman A.;
 RT "Developmental expression of the protein product of Vg1, a localized maternal mRNA in the frog *Xenopus laevis*.";
 RL EMBO J. 8:1057-1065(1989).
 RP -!- FUNCTION: SERVES TO FACILITATE THE DIFFERENTIATION OF EITHER MESODERM OR ENDODERM EITHER AS A COFACTOR IN AN INSTRUCTIVE SIGNAL OR BY PROVIDING PERMISSIVE ENVIRONMENT.
 CC -!- SUBUNIT: Homodimer (Probable)
 CC -!- TISSUE SPECIFIC: VEGILL REGION OF THE EGG.
 CC -!- DEVELOPMENTAL STAGE: ABUNDANT IN OOCYTES AND PRESENT THROUGHOUT CLEAVAGE AND GASTRULATION STAGE. NOT READILY DETECTED AT A STAGE WHEN SOMITogenesis IS NEARLY COMPLETE IN 24 HR EMBRYOS. STEADY STATE LEVEL DECREASES IN A CONTINUOUS FASHION WITH DEVELOPMENTAL AGE.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.

RESULT 14

BMBB_MOUSE STANDARD; PRT; 360 AA.
 ID BMBB_MOUSE STANDARD; PRT; 360 AA.
 AC P55105;
 DT 01-OCT-1996 (Rel. 34; Created)
 DT 01-OCT-1996 (Rel. 34; Last sequence update)
 DT 15-MAR-2004 (Rel. 43; Last annotation update)
 DE Bone morphogenetic protein 8B precursor (BMP-8B).
 GN BMP8B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10909;
 RN [1]
 RP SEQUENCE FROM N_A.
 RC STRAIN=ICR; TISSUE=Placenta;
 RX MEDLINE=9700308; PubMed=8843393;
 RA Zhao G.-Q., Hogan B.-L.;
 RT "Evidence that mouse Bmp8a (Op2) and Bmp8b are duplicated genes that play a role in spermatogenesis and placental development.";
 RC Mech. Dev. 57:159-168(1996);
 CC -!- FUNCTION: Induces cartilage and bone formation. May be the osteoinductive factor responsible for the phenomenon of epithelial-mesenchymal transition. Plays a role in calcium regulation and bone homeostasis (By similarity).
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.

FT VARIANT 59 V -> G (IN STRAIN DP CN BW).
FT VARIANT 121 K -> M (IN STRAIN DP CN BW).
FT VARIANT 473 H A -> QP (IN STRAIN DP CN BW).
SEQUENCE 588 AA; 65850 MW; 3D98A7DF66B CRC64;

Query Match 64.0%; Score 71; DB 1; Length 598;
Best Local Similarity 55.0%; Pred. No. 0.0037;
Matches 11; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IMPETVKPCGPTQLNAIS 20
Db 543 MNP3KVPKACCVPTQLDSVA 562

Search completed: October 12, 2004, 09:34:23
Job time : 20 secs

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